requirement. Indeed, the Examiner conceded that her Supervisor was somewhat sympathetic to Applicants' position. As a result, a tentative agreement on an approach to respond to the outstanding election of species requirement was reached.

The Examiner should recall that claim 7 is directed to a two-step process as follows:

Claim 7 A method for producing a genomic DNA library, comprising the steps of

(1) subjecting a genomic DNA to DNA fragmentation means for generating a mixture of fragmented DNAs having distribution ratio of 1 to 5 as defined by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA and having a size convergence rate of 80% or more, thereby giving a mixture of fragmented DNAs; and

(2) subjecting the mixture of fragmented DNAs obtained in step (1) to nucleic acid amplification, thereby producing DNAs corresponding to said mixture of fragmented DNAs, to give a genomic DNA library maintaining substantially copy numbers of a set of genes or sequences on a genomic DNA and an abundance ratio of said set of genes or sequences on the genomic DNA.

Applicants agree to elect a species from group b), which refers to a "DNA fragmentation means," since this is the active step of step (1). The type of "DNA fragmentation means" that Applicants elect is recited in claim 8. Claim 8 recites that said

"DNA fragmentation means" is physical means. If the Examiner believes that the election of a physical means is non-responsive, then Applicants further elect a hydrodynamic point-sink shearing method as recited in claim 9.

Accordingly, since claim 7 recites a process and the first step of the process (e.g. step (1)) generates a mixture with a DNA fragmentation means, then Applicants respectfully submit that the election of a hydrodynamic point-sink shearing method as recited in claim 9 is fully responsive to the election with respect to step (1).

Applicants agree to elect a species of "nucleic acid amplification" of Group e) since this is the active step of step (2) and since it is a generic term encompassing many types of "nucleic acid amplification." That is, Applicants elect nucleic acid amplification which uses a mixture of DNA polymerase having 3' → 5' exonuclease activity and a DNA polymerase having no 3' → 5' exonuclease activity.

Moreover, amplification primers of Group d) are used in step (2) of claim 7. However, since the primers correspond to the genomic DNA, the sequences of these primers are not limited to any specific sequence. [The traversal of the requirement of an election of a species of genomic DNA is discussed below.]

Accordingly, since claim 7 recites a process and the second step of the process (e.g. step (2)) subjects the mixture of

fragmented DNAs obtained in step (1) to nucleic acid amplification, then Applicants respectfully submit that the election of a mixture of DNA polymerase having 3′ → 5′ exonuclease activity and a DNA polymerase having no 3′ → 5′ exonuclease activity is fully responsive to the election with respect to step (2).

Applicants have elected specific species for the active process steps for each of steps (1) and (2) of claim 7. The remaining elections within the various groups are not believed to be at all reasonable under any standard of election practice.

The Examiner's requirement of a specific genomic DNA sequence of Group a) is traversed since the process of claim 7 is independent of the type of genomic DNA sequence starting material. Applicants are not claiming any particular type of genomic DNA sequence, so the election is improper. That is, the selection of a species of genomic DNA sequence as a starting material is not limited to any particular species of genomic DNA. The invention is directed to a process manipulating any type of genomic DNA in accordance with the two steps set forth in claim 7.

Similarly, the choice of any particular ligase of Group c) is traversed since Applicants are not claiming a ligase.

The selection of species for Groups f) - i) of claim 16 is traversed with respect to claim 7 since these Groups further define sequences for the amplification primers and depend on the genomic

DNA. The sequences of these primers are not limited to any specific sequence.

During the interview, Applicants' representatives indicated to the Examiner that the above information is all that is reasonably required in response to the election of species requirement. The Examiner understood Applicants' position and suggested that Applicants make their election along with their traversal.

Should there be any outstanding matters that need to be resolved in the present application, the Examiner is respectfully requested to contact Marc S. Weiner (Reg. No. 32,181) at the telephone number of the undersigned below, to conduct an interview in an effort to expedite prosecution in connection with the present application.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

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Respectfully submitted,

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